

Effects of Fermentative Activity on Fate and Transport of U and Cr

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ERSP PI Meeting 2008



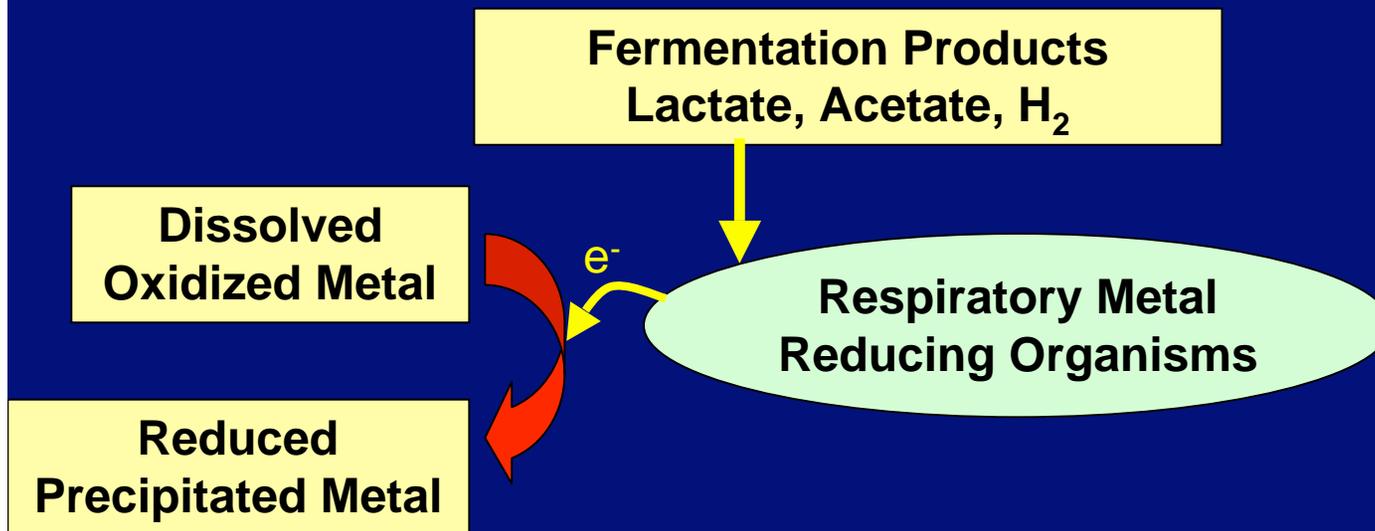
 Center for
Biofilm
Engineering



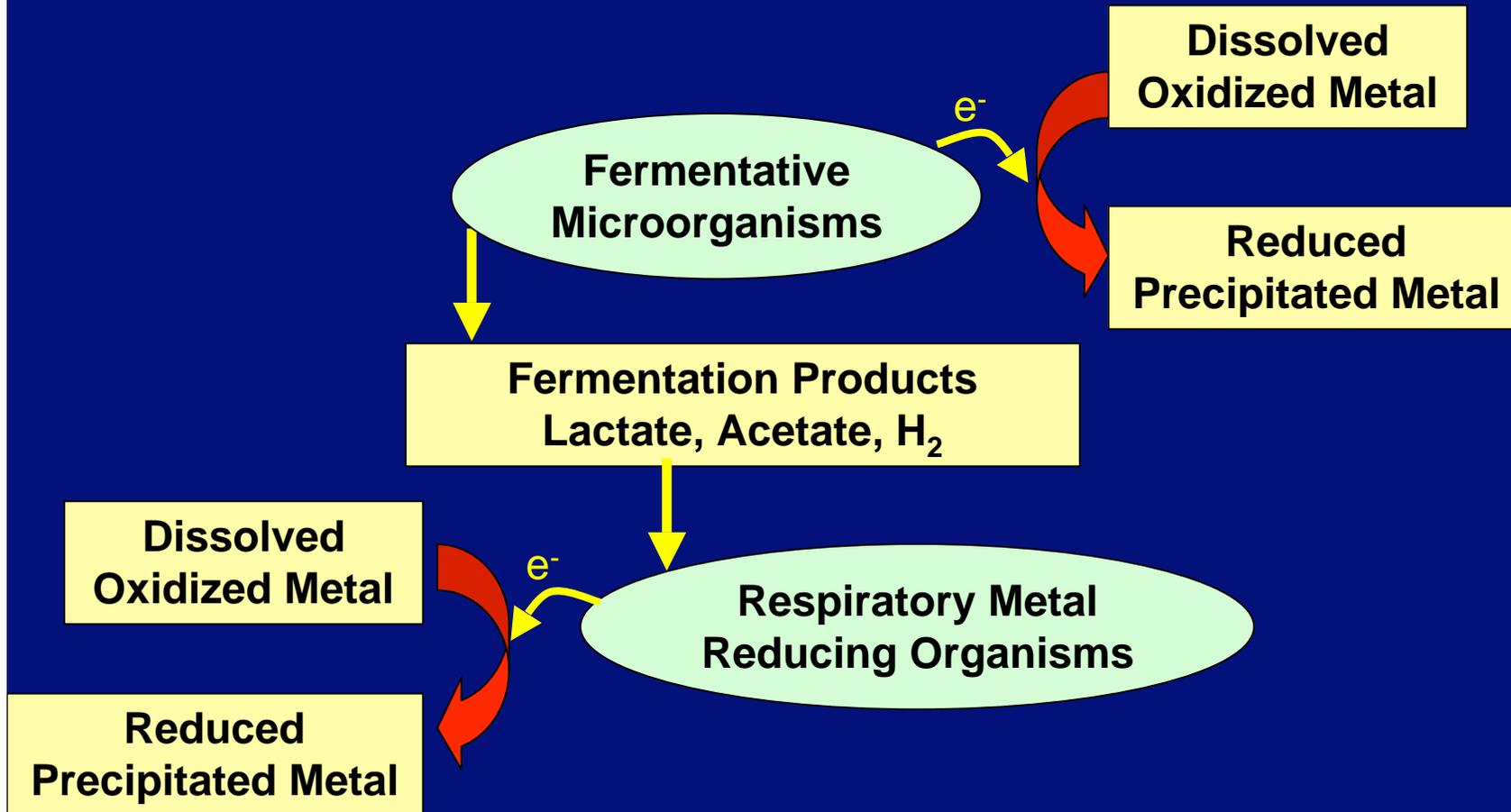
Acknowledgements

- Thomas Borch, CSU
- Amber Miller, INL
- Rajesh Sani, SDSMT
- Bill Smith, INL
- Alice Dohnalkova, PNNL
- Andy Neal, SREL/UGA
- Gary Anderson, LBNL
- Yvette Piceno, LBNL
- Erin Field, MSU
- Vaidee Sivaswamy, WSU
- Mike VanEngelen, MSU
- Sridhar Viamajala, USU
- DOE Environmental Remediation Science Program
- Inland Northwest Research Alliance
- Advanced Photon Source, Argonne National Laboratory

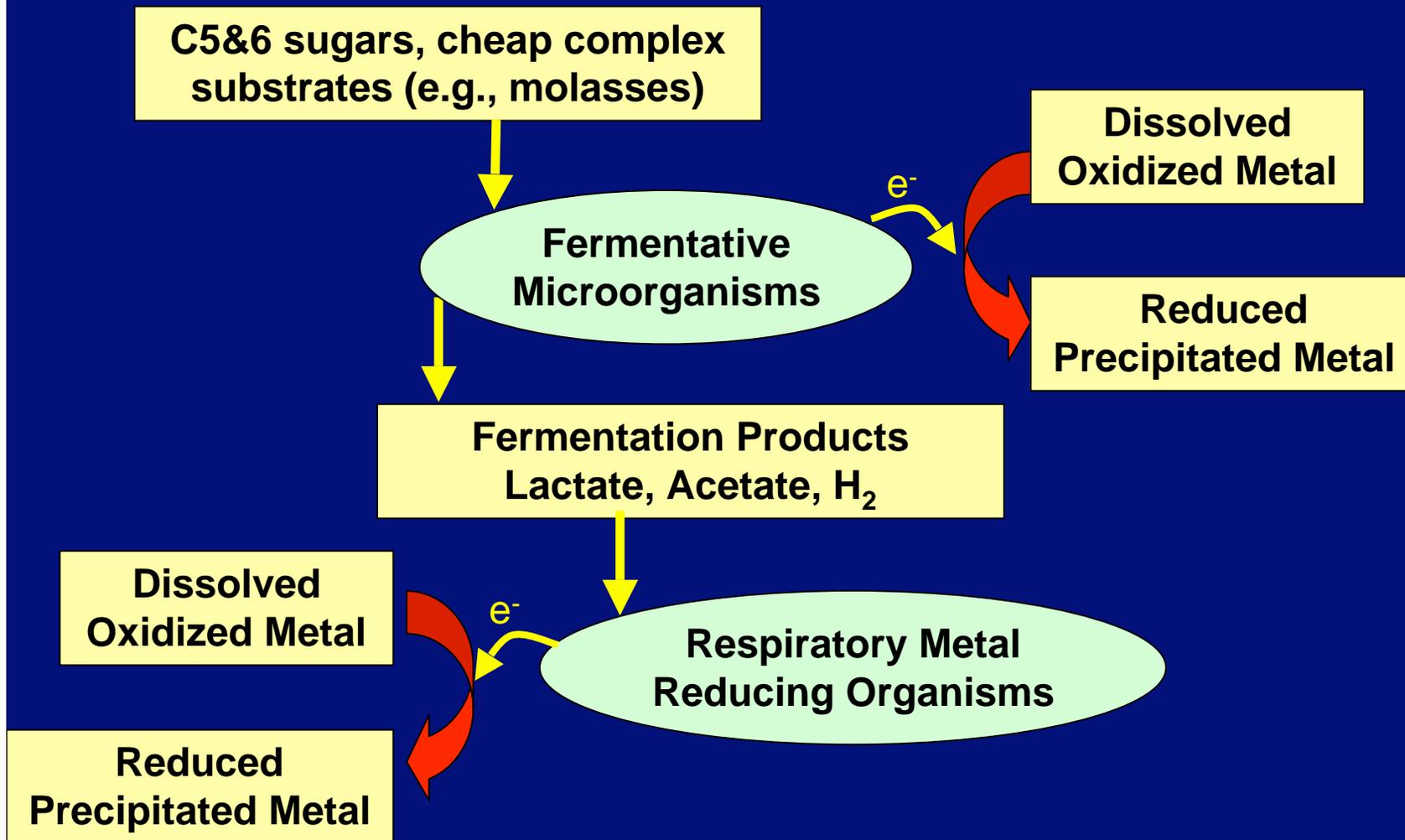
Microbial Metal Transformations



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Background

- Cr(VI) impacted core from 100-D area borehole (DOE Hanford facility in southeastern Washington State), designated groundwater monitoring well 199-D2-8



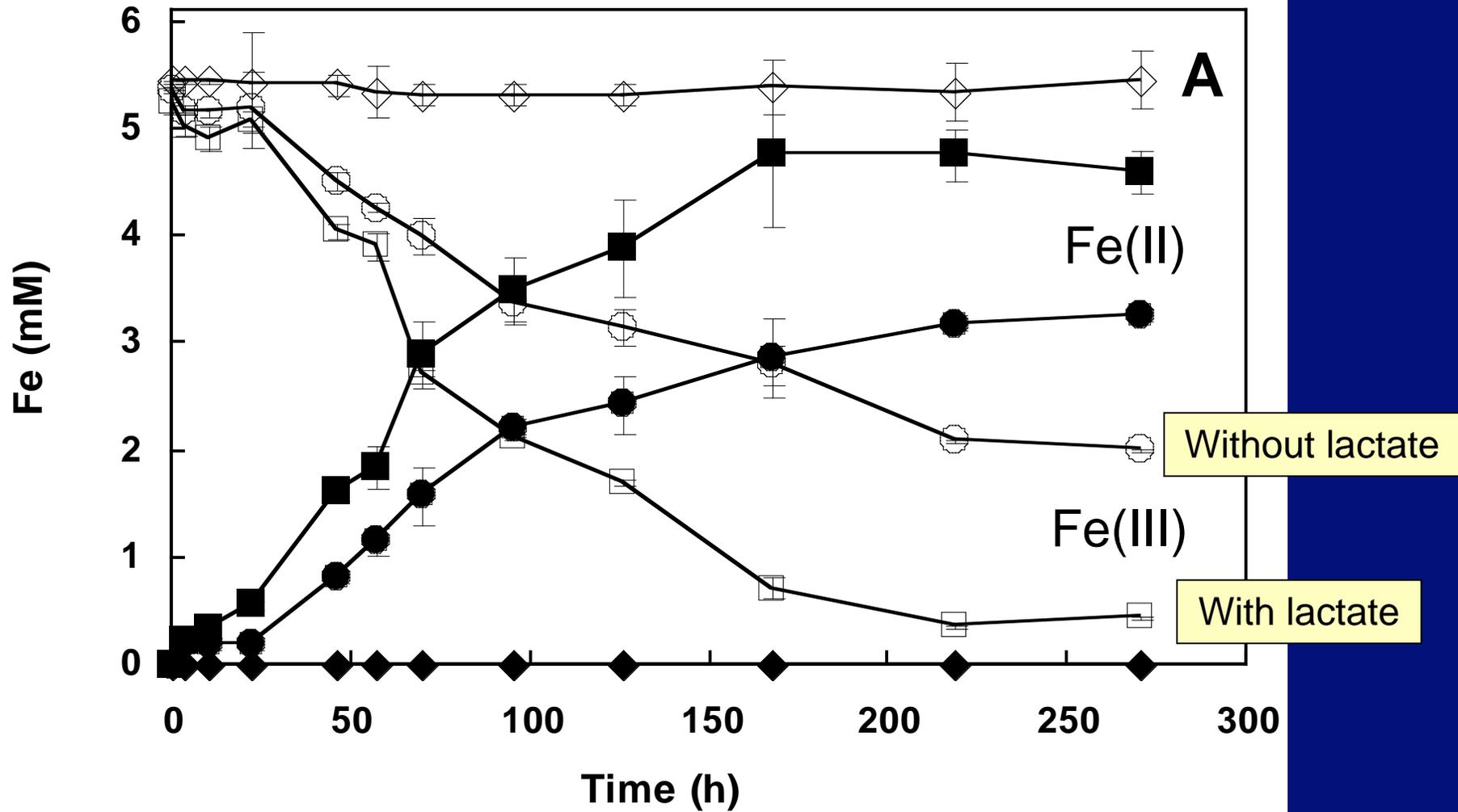
Background

- Cr(VI) impacted core from 100-D area borehole (DOE Hanford facility in southeastern Washington State), designated groundwater monitoring well 199-D2-8
- Sedimentary flood deposits described as loosely consolidated fine-grained sand and silt (Lindsey and Jaeger, 1993)
- The water table was 24.8m bgs. Sediment samples taken from Ringold Formation at 23.3m and 25.9m bgs.
- Enrichments grown in the presence of Cr(VI) and nitrate - with acetate, D-xylose or glycerol as a carbon and energy source.

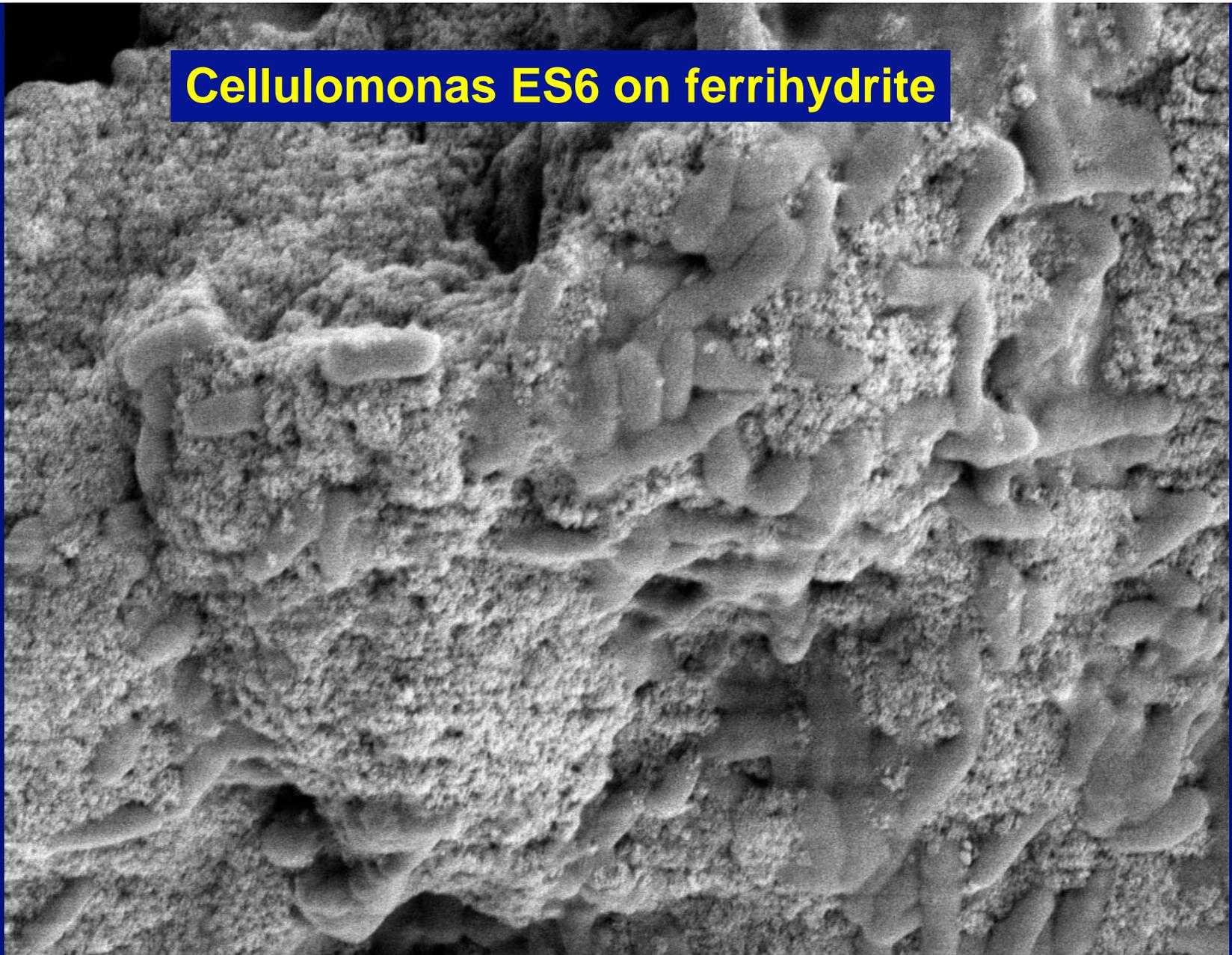
Rep. Strain1	RDP II2		Isolates found			
	Closest match	Similarity index ³	26m-X	23m-X	23m-G	ES
WS01	<i>Cellulomonas turbata</i>	0.856	—	—	—	—
WS12	<i>Cellulomonas</i> sp. str. 1533	0.954	—	—	—	—
WS18	<i>Cellulomonas turbata</i>	0.811	—	—	—	—
ES6	<i>Cellulomonas hominis</i>	0.933	—	—	—	—
WS06	<i>Sanguibacter inulinus</i>	0.996	—	—	—	—
WS08	1397 clone SB-22	0.972	—	—	—	—
WS10	<i>Pseudomonas brassicacearum</i>	0.953	—	—	—	—
WS19	Marine snow bacterium	0.712	—	—	—	—
WS13	<i>Arthrobacter</i> sp. str. S2	0.771	—	—	—	—

- 8 of 9 isolated strains were Gram positive
- 4 were identified by 16S rRNA sequence and membrane fatty acid composition as belonging to the genus *Cellulomonas*

Fe(III) Reduction



Cellulomonas ES6 on ferrihydrite

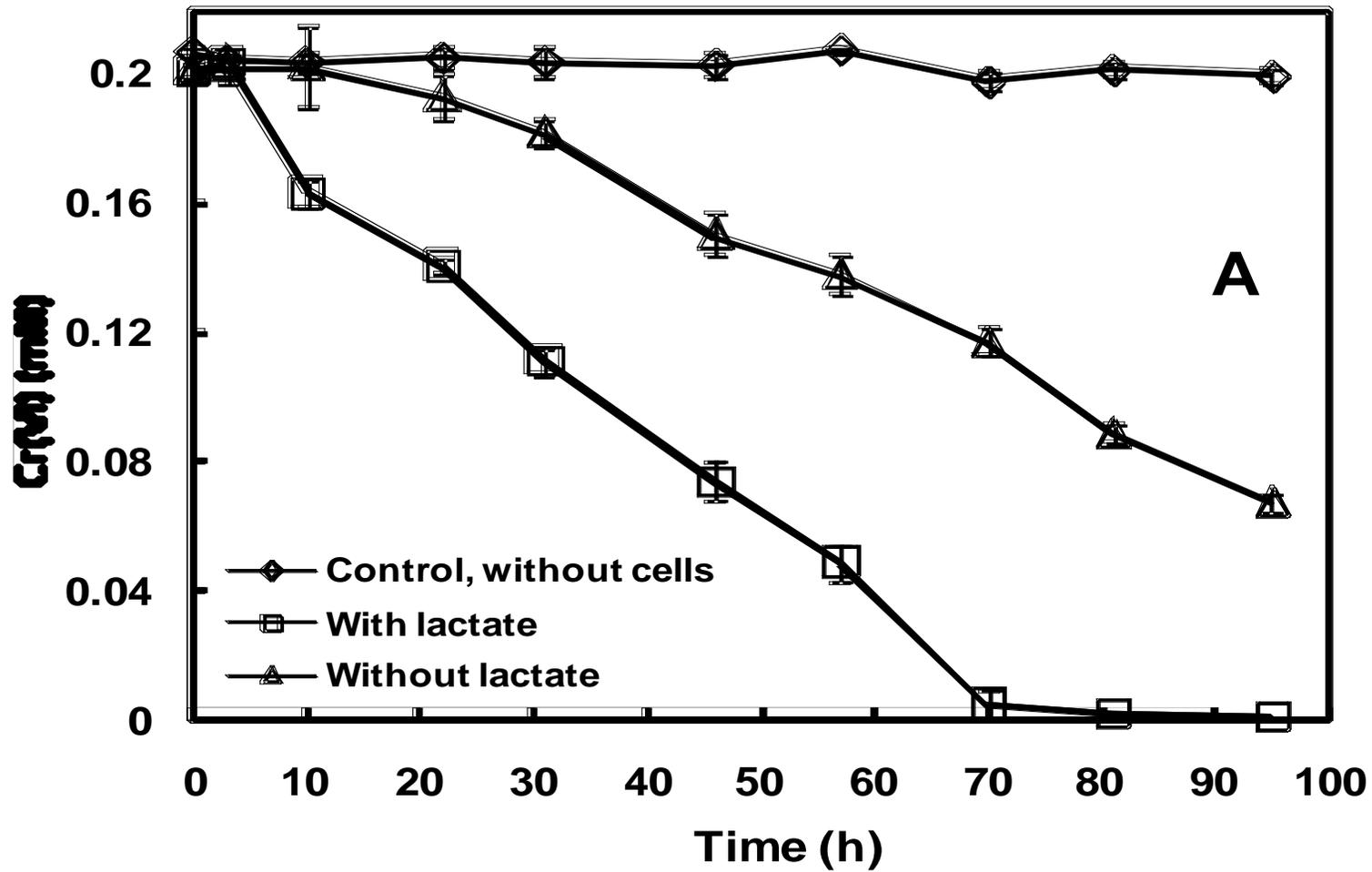


x10000
#41 3
1024 x 960

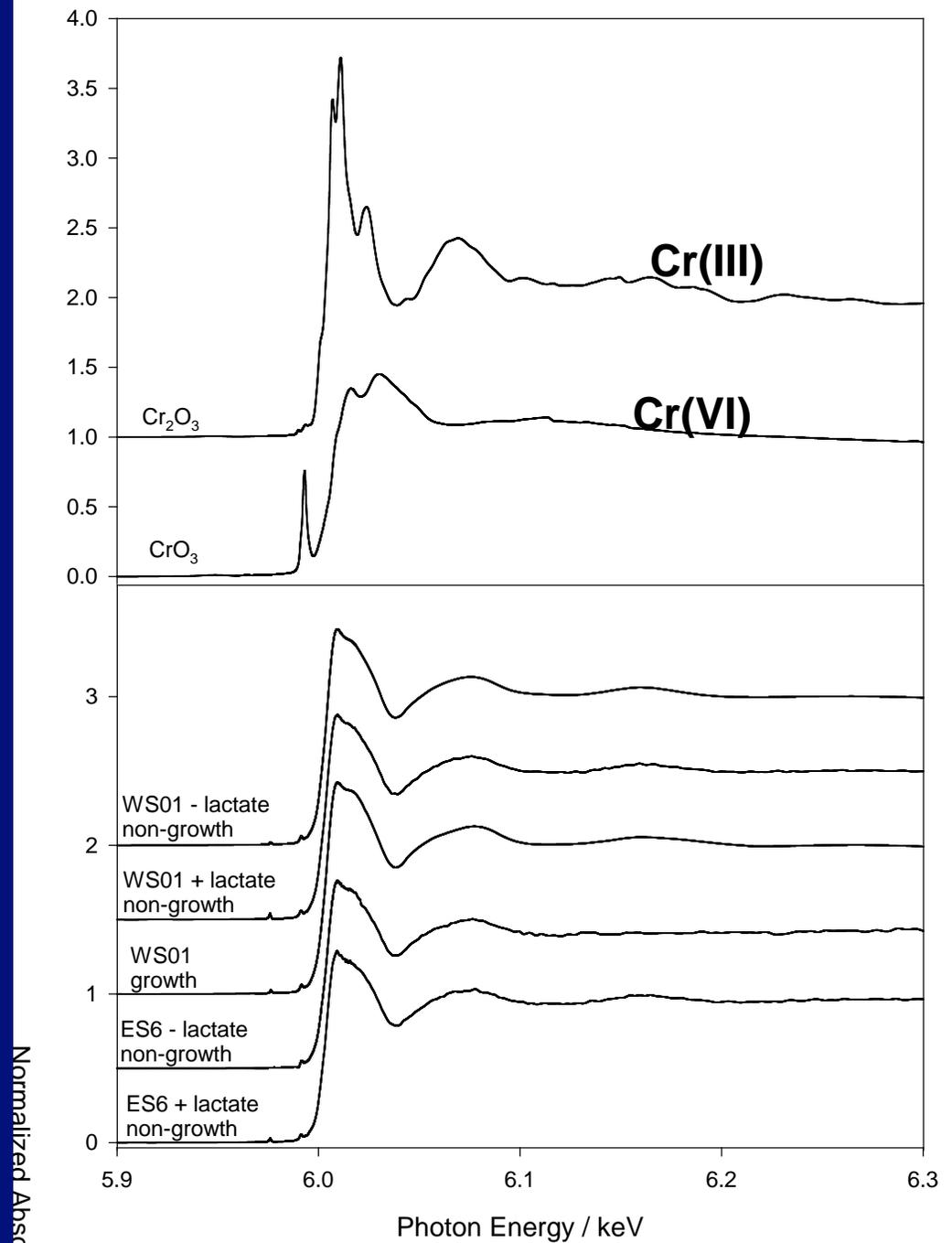
2 μ m

3.00kV 10mm
2-10-03
L3-2.TIF

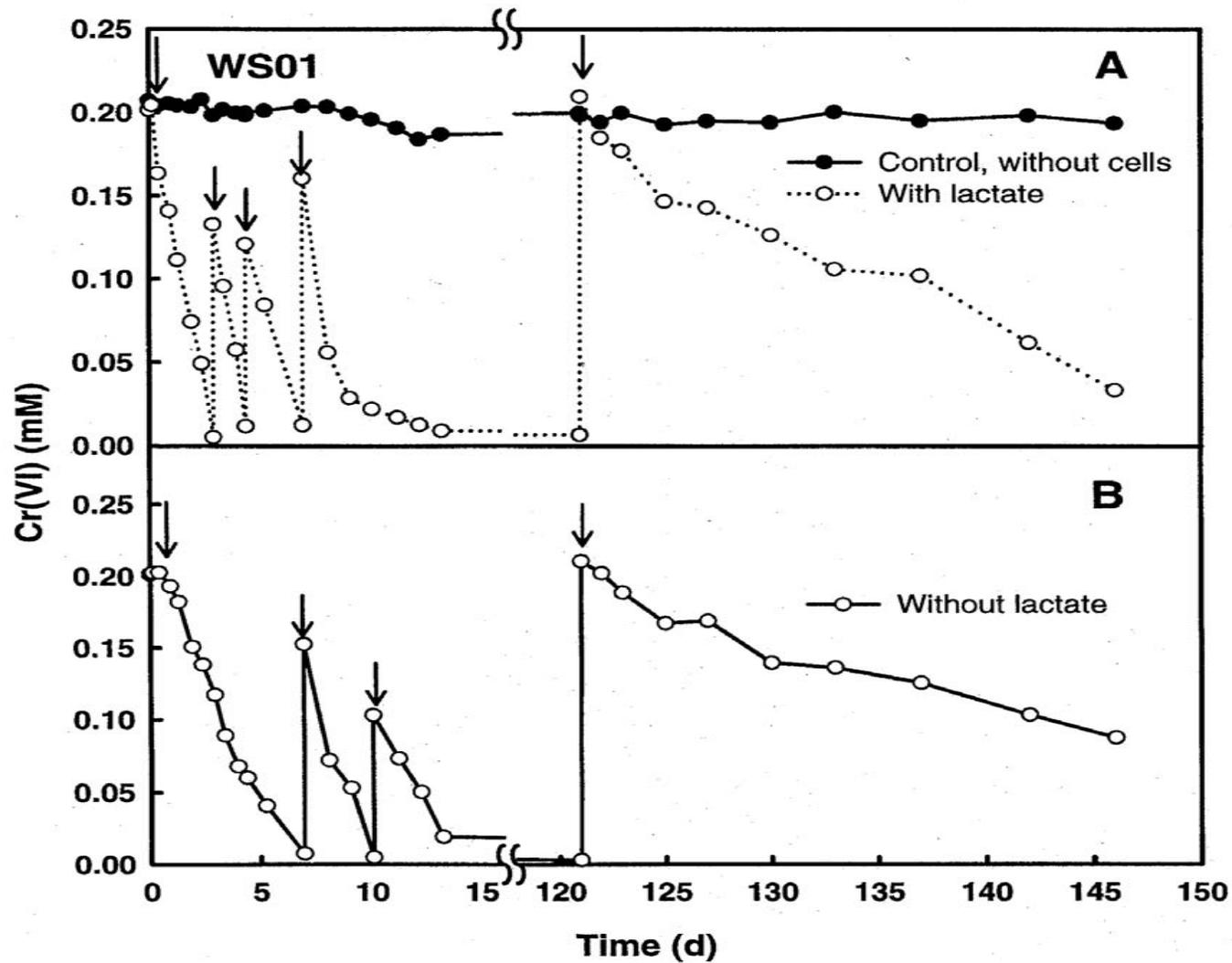
Cr(VI) Reduction



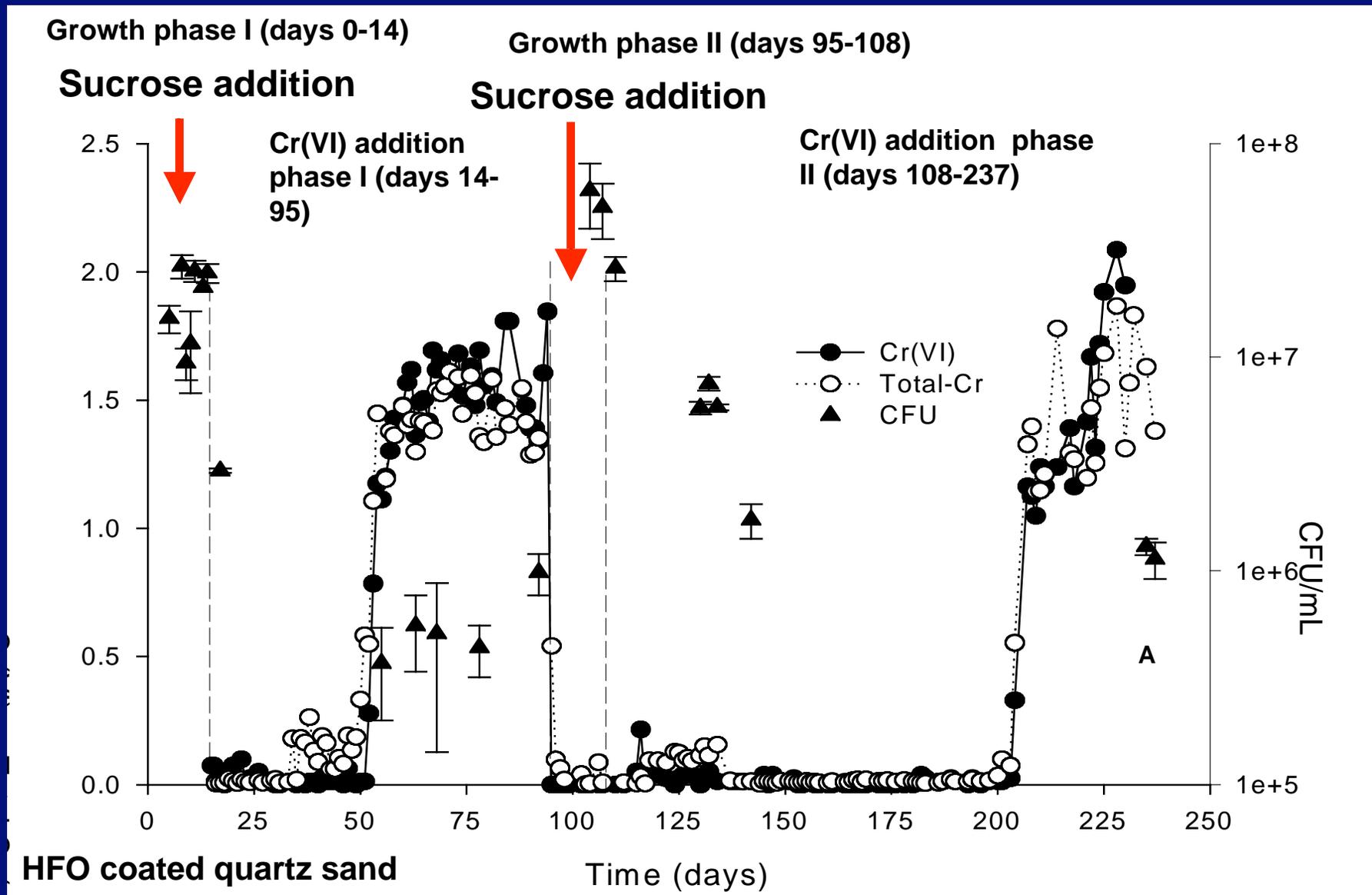
Cr K-edge X-ray
absorption
near-edge spectroscopy
(XANES) spectra indicate
that Cr(VI) was reduced
to Cr(III) form.



Long Term Cr(VI) Reduction

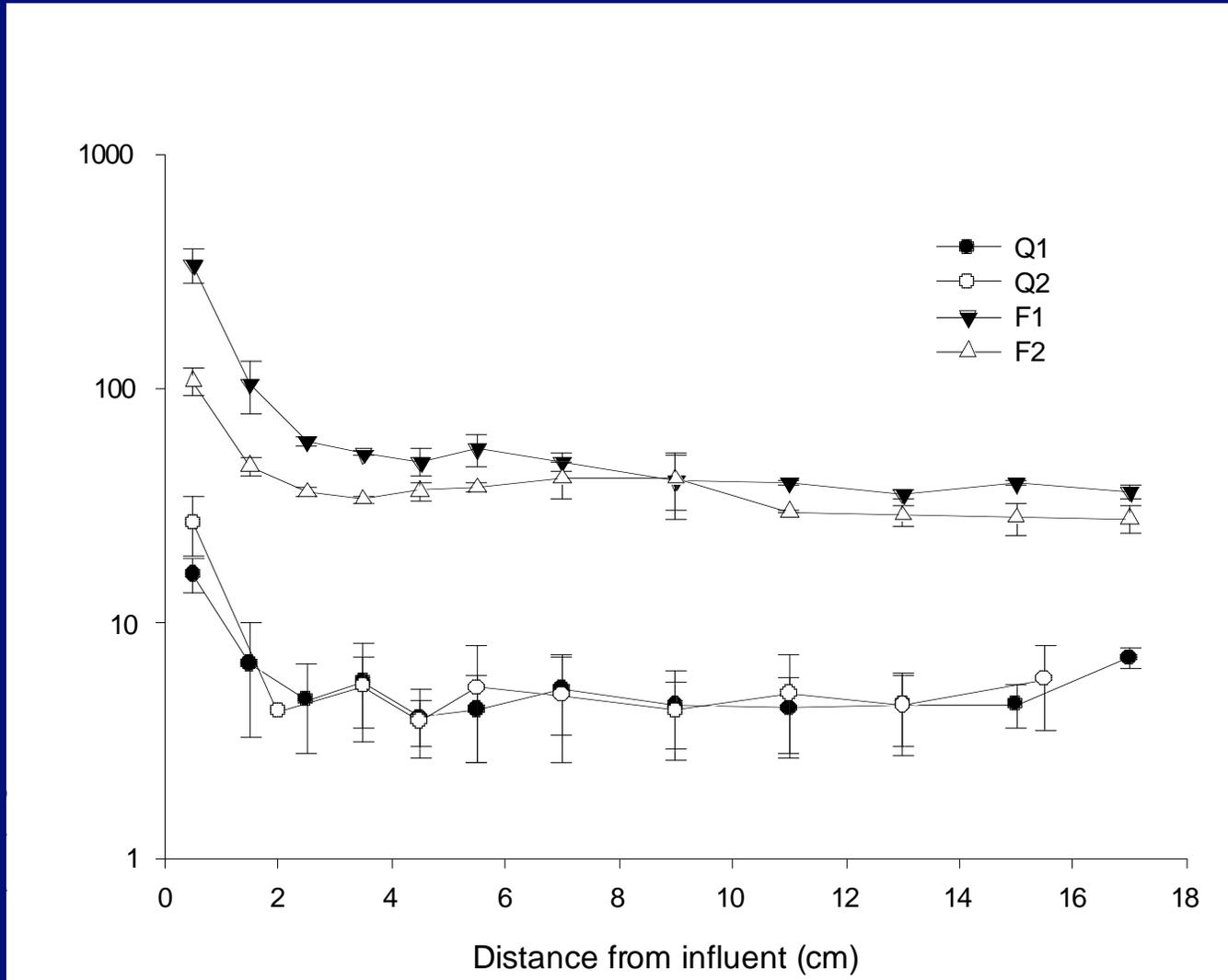


Long Term Flow Studies



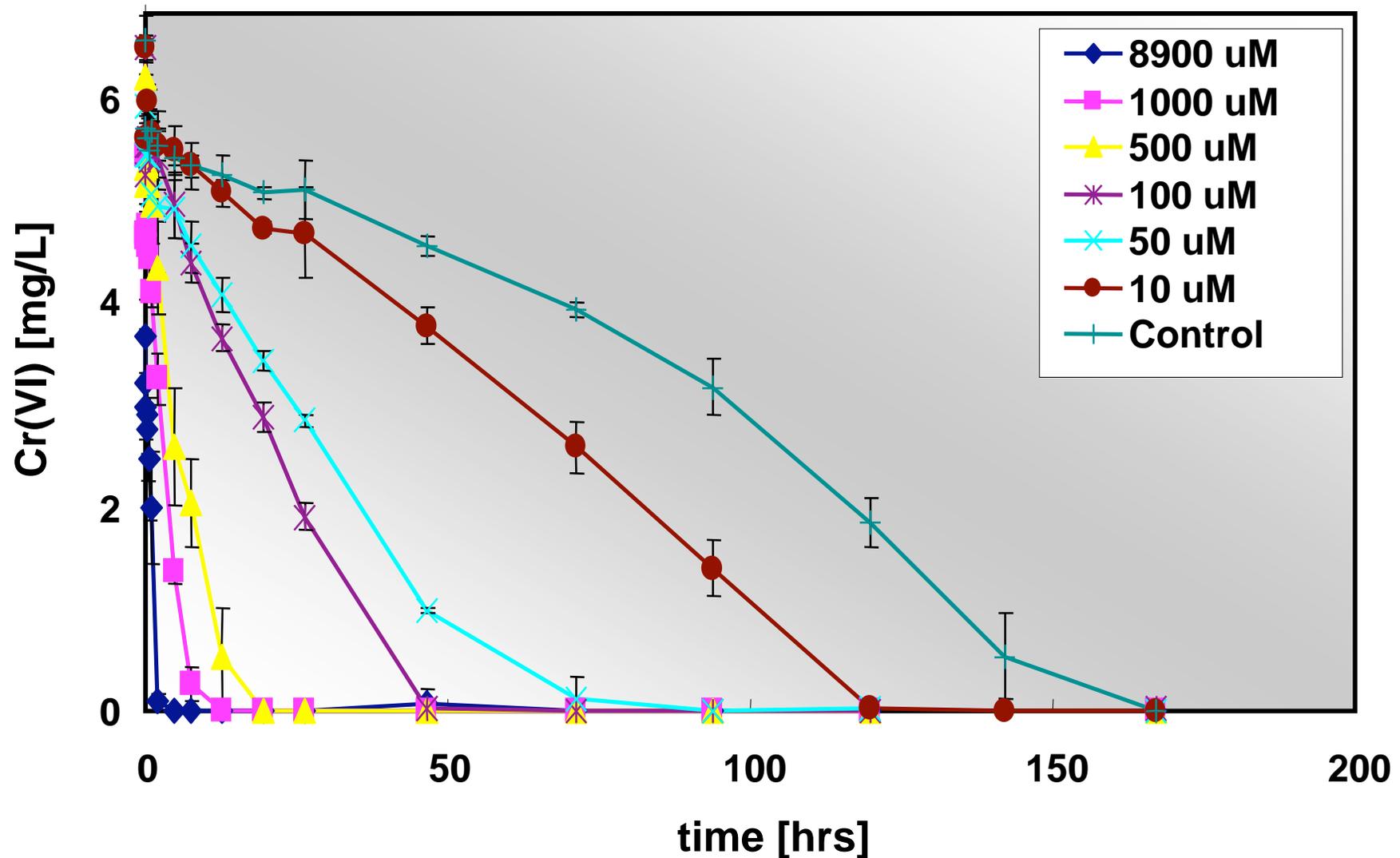
Submitted to Biotech. Bioeng., Permeable reactive biobarriers for *in-situ* Cr(VI) reduction: Bench scale tests using *Cellulomonas* sp. strain ES6. S. Viamajala, B.M. Peyton, R. Gerlach, V. Sivaswamy, W.A. Apel, J.N. Petersen

Solid Phase Cr Accumulation



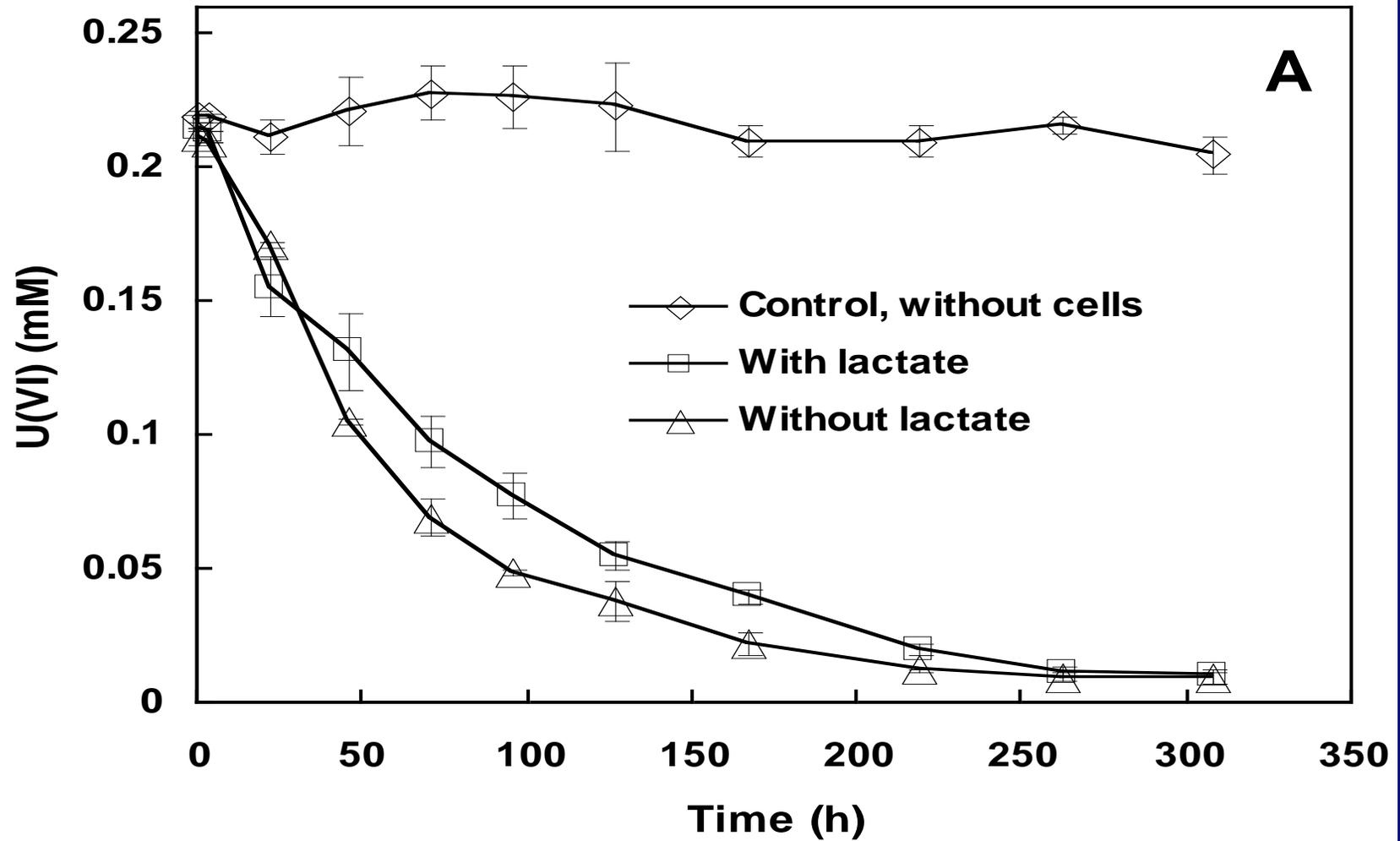
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Cr(VI) Reduction - ES6 w/AQDS



e⁻ donor =

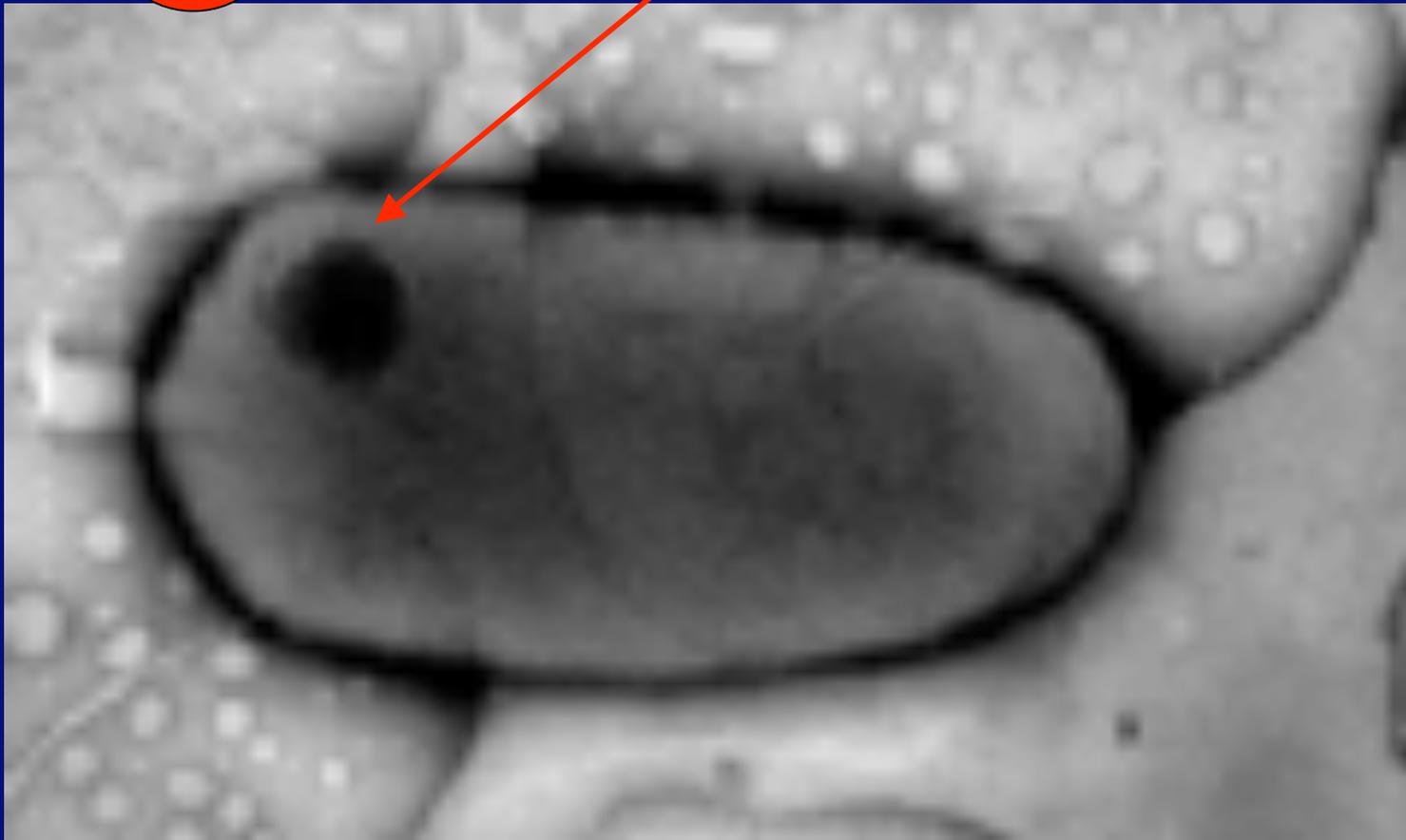
U(VI) reduction ?



Energy Storage Compounds?

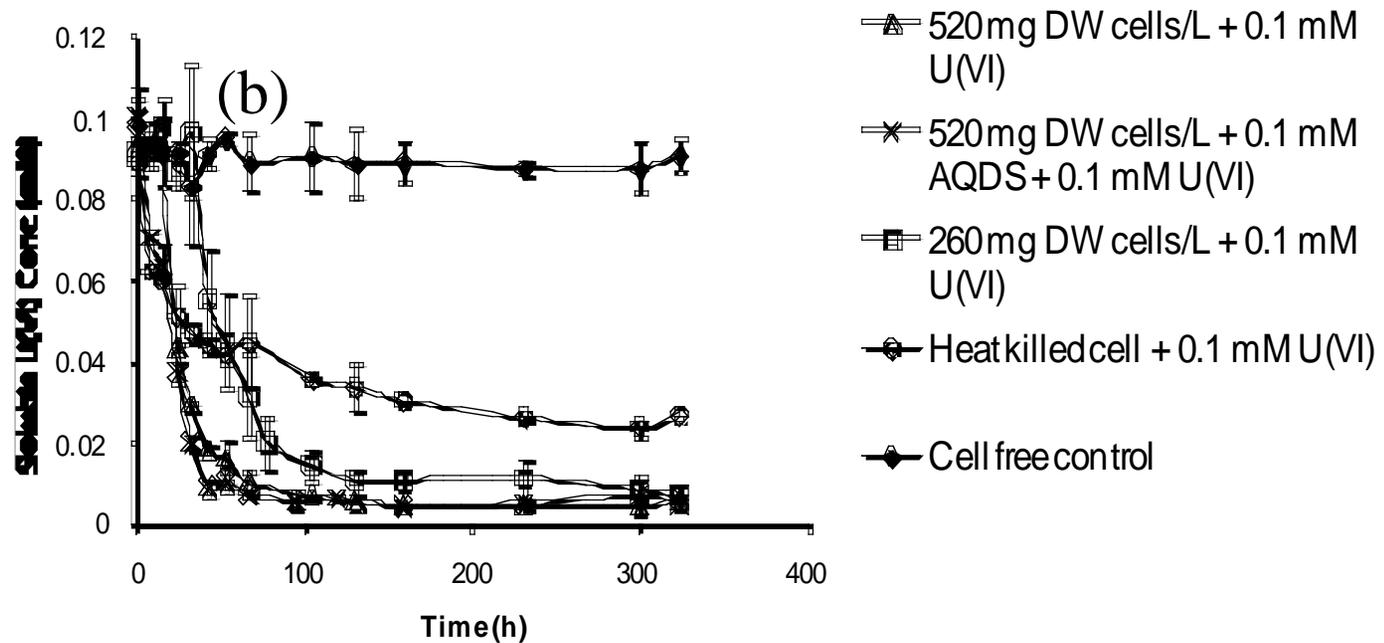
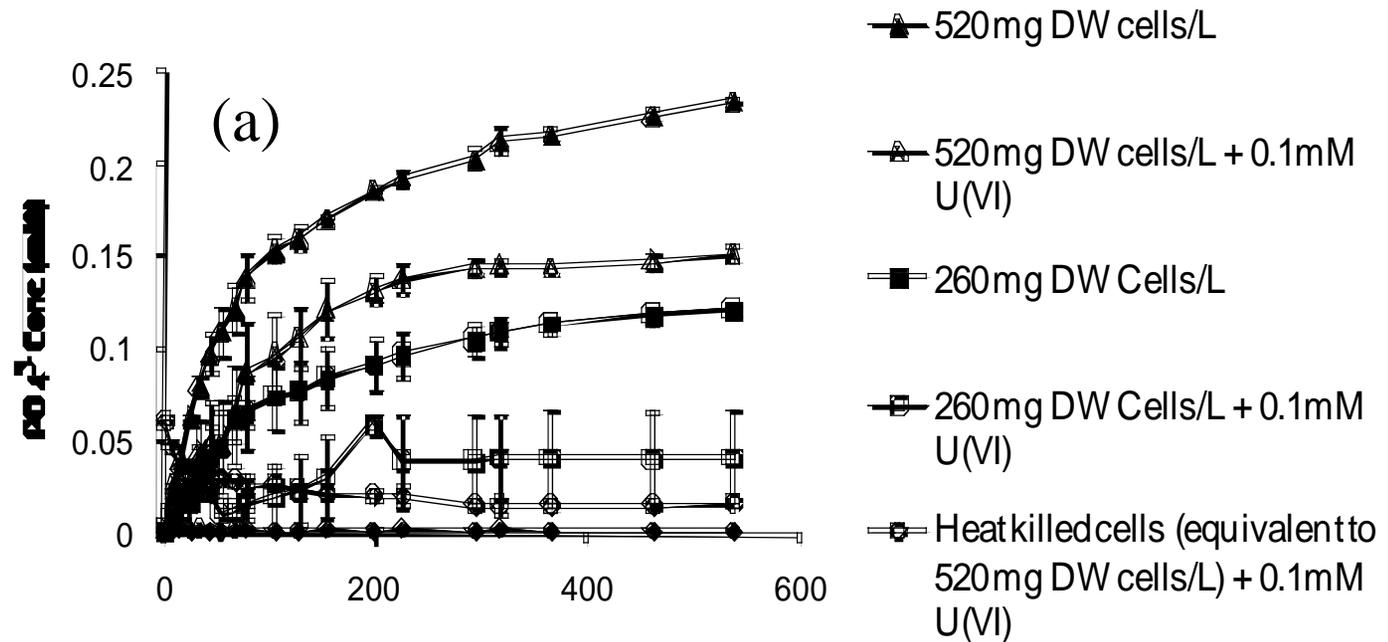
- Polyhydroxybutyrate (PHB)
- Trehalose

- Polyphosphate

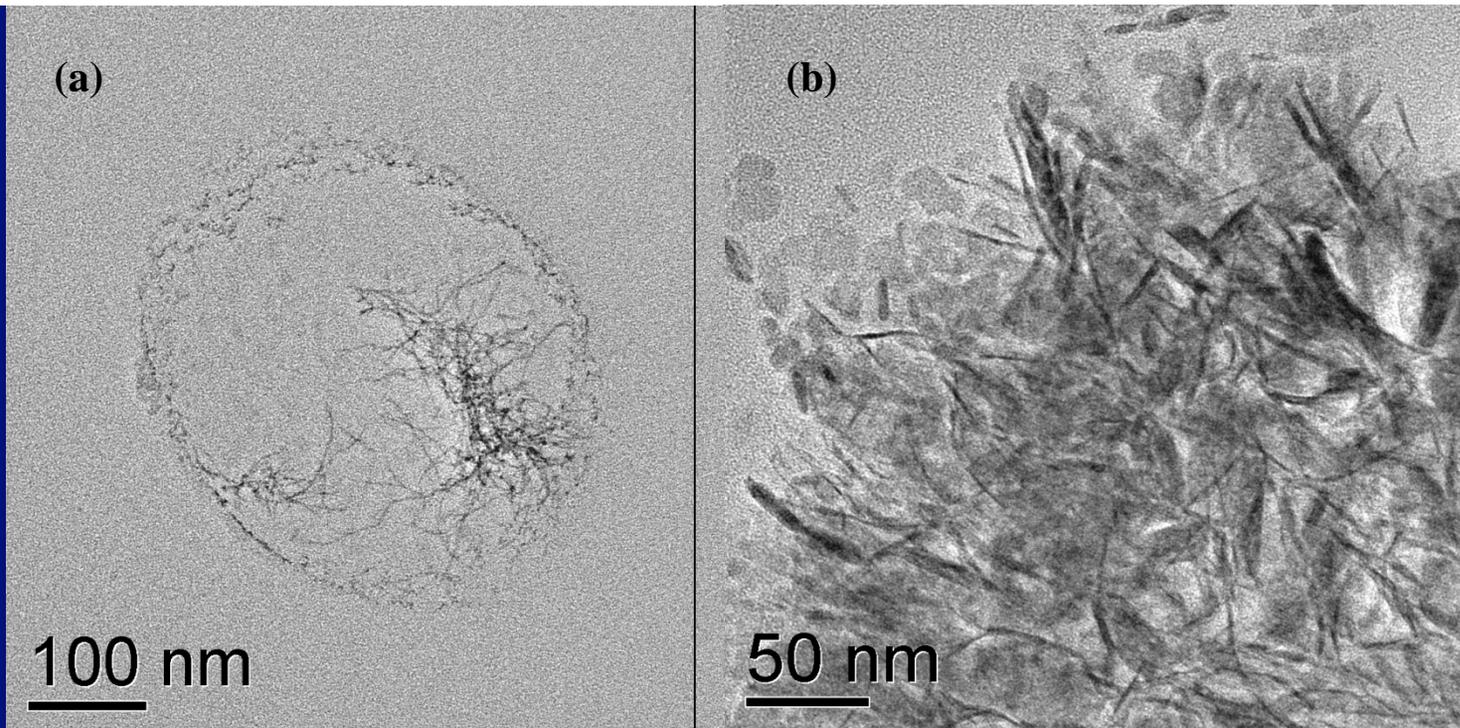




PIPES
Buffer
(30mM)

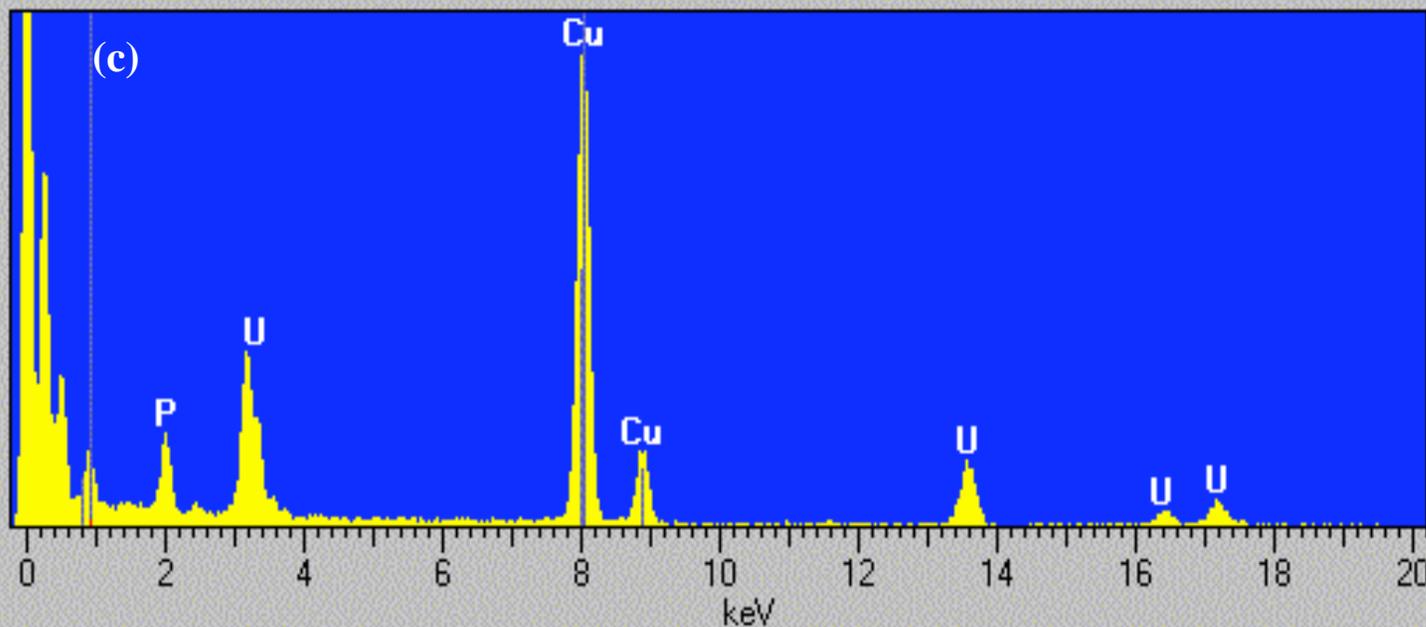


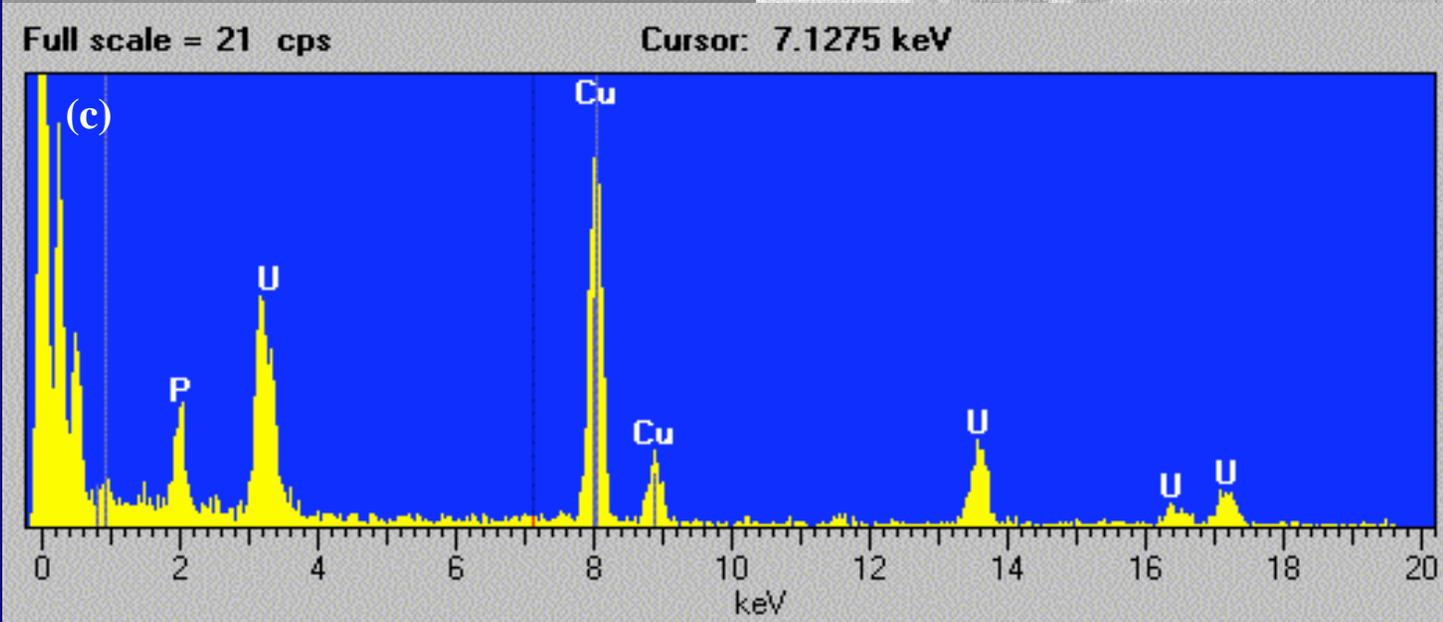
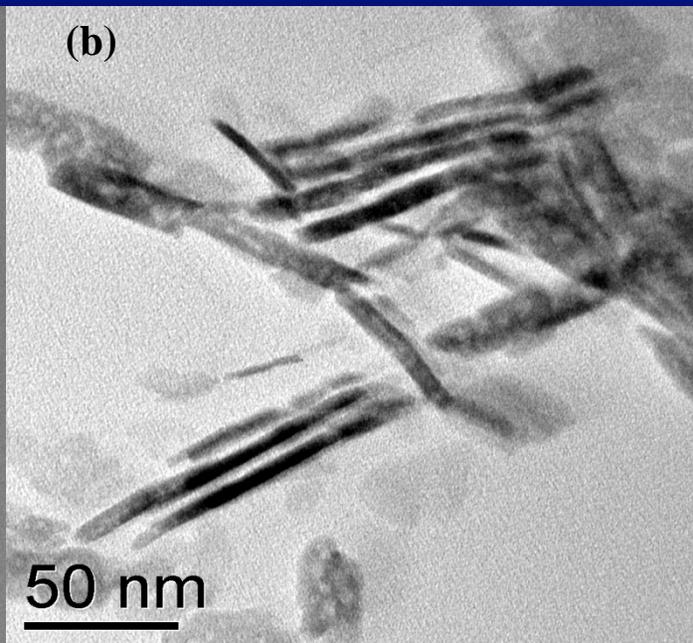
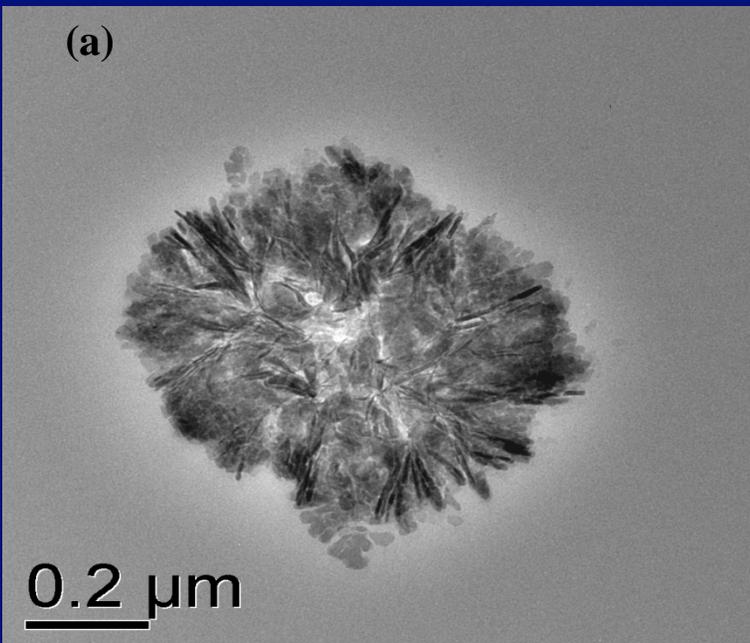
**HR-TEM w/
elemental
analysis
indicates
that U &
phosphate
was
precipitating
both inside
and outside
the cell.**



Full scale = 25 cps

Cursor: 0.9275 keV

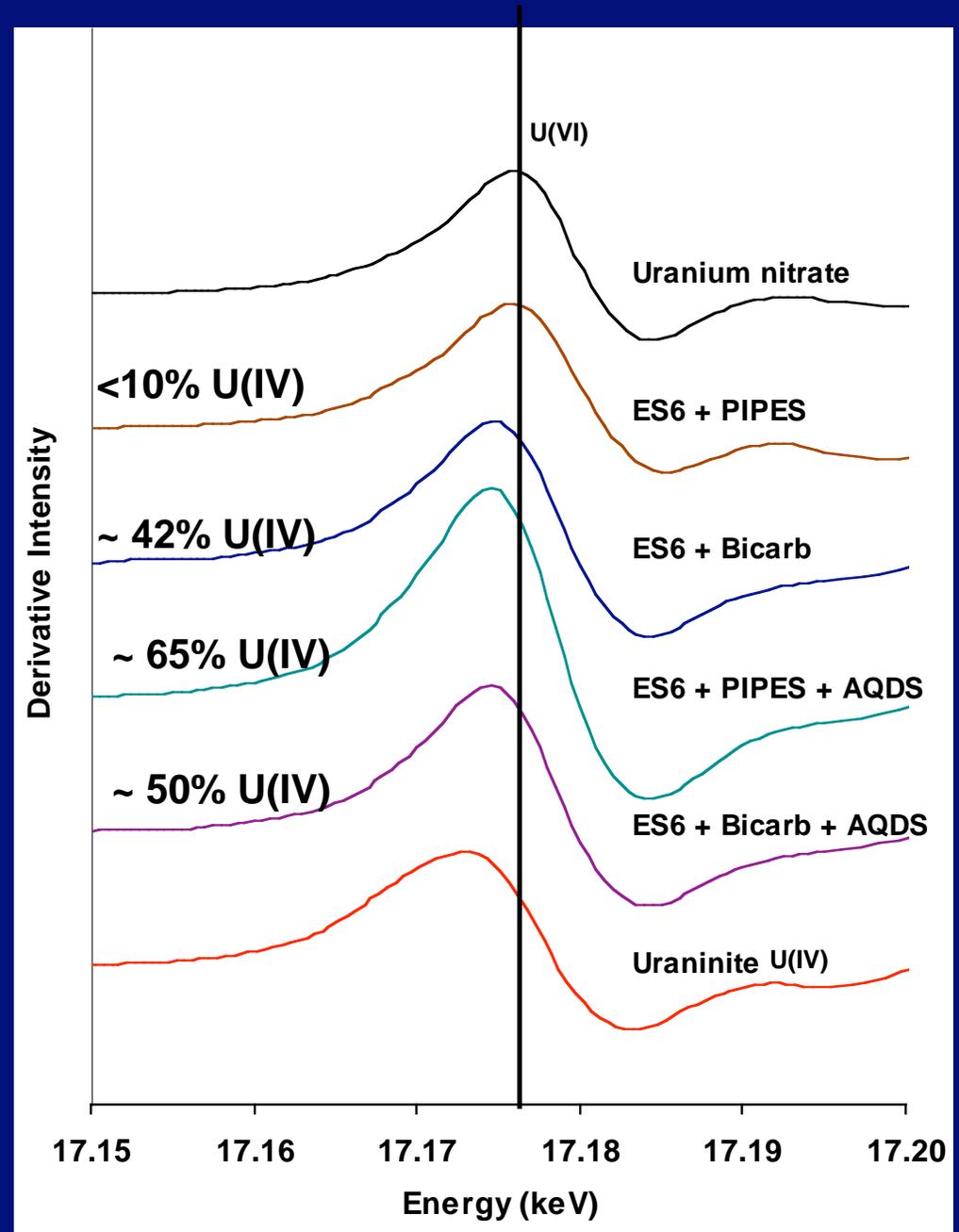




Uranium Solids

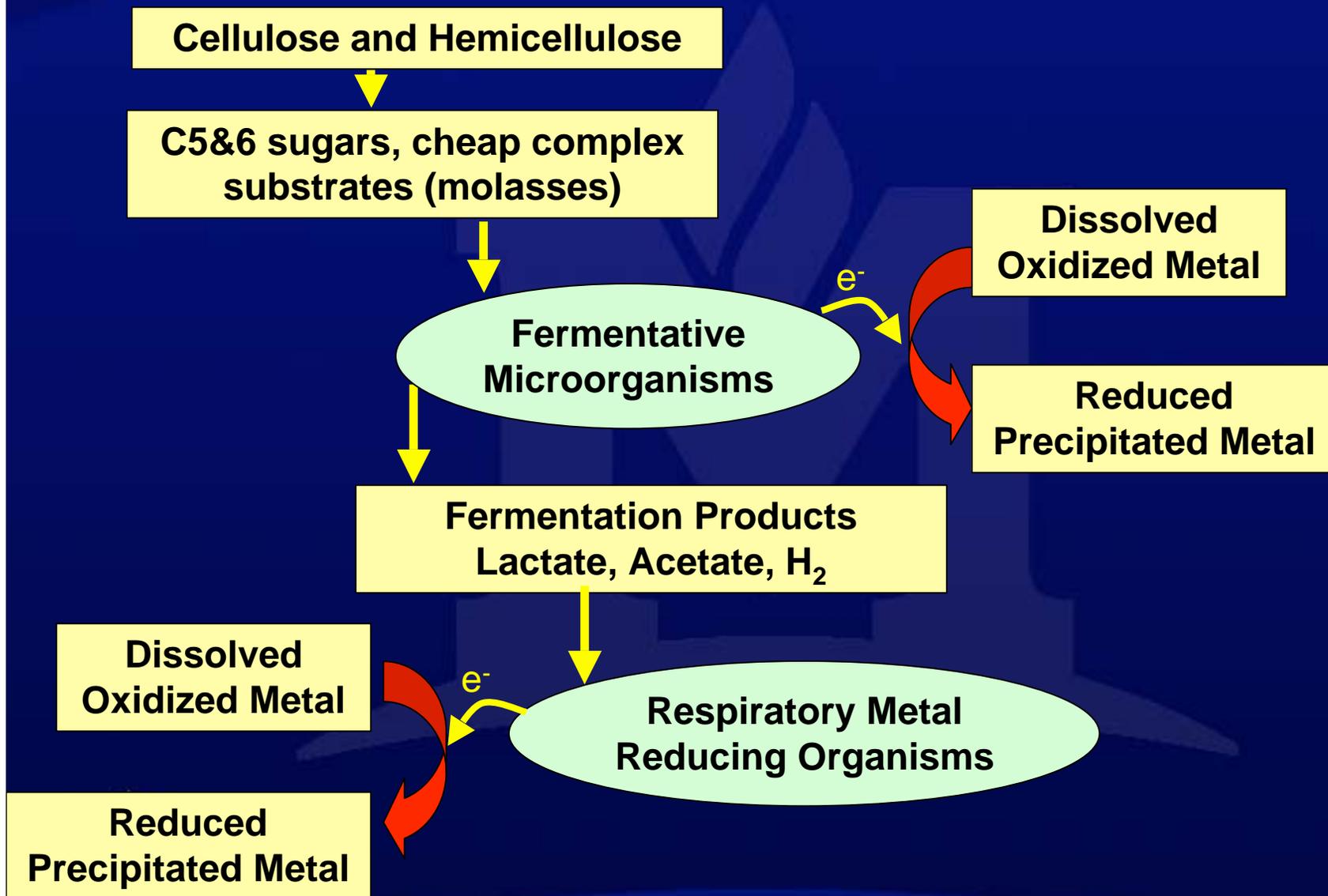
First derivative X-ray absorption near edge structure (XANES) spectra of uranium precipitates.

The buffer and the presence or absence of AQDS affected the U(IV):U(VI) ratio.

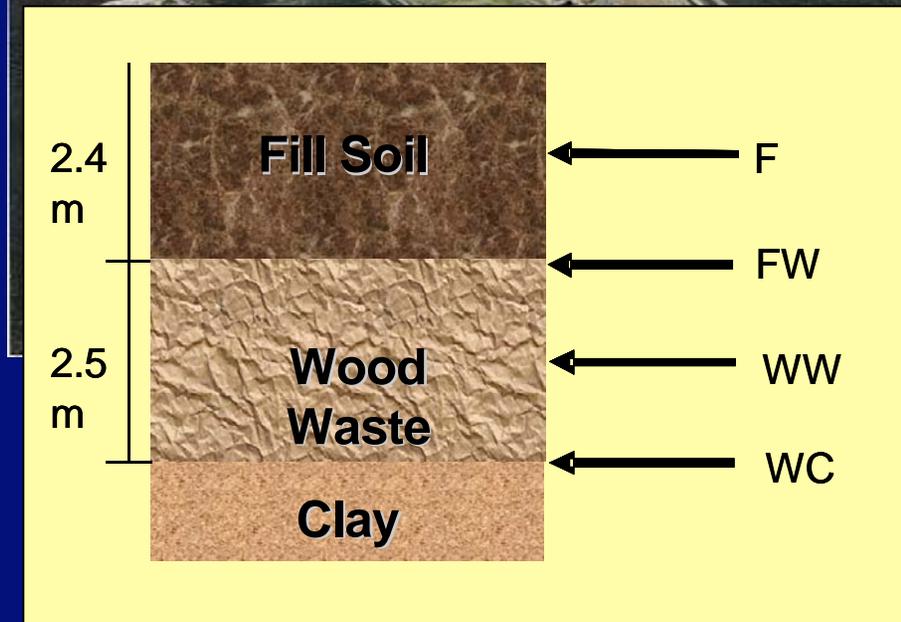


Thomas Borch, CSU

Microbial Metal Transformations



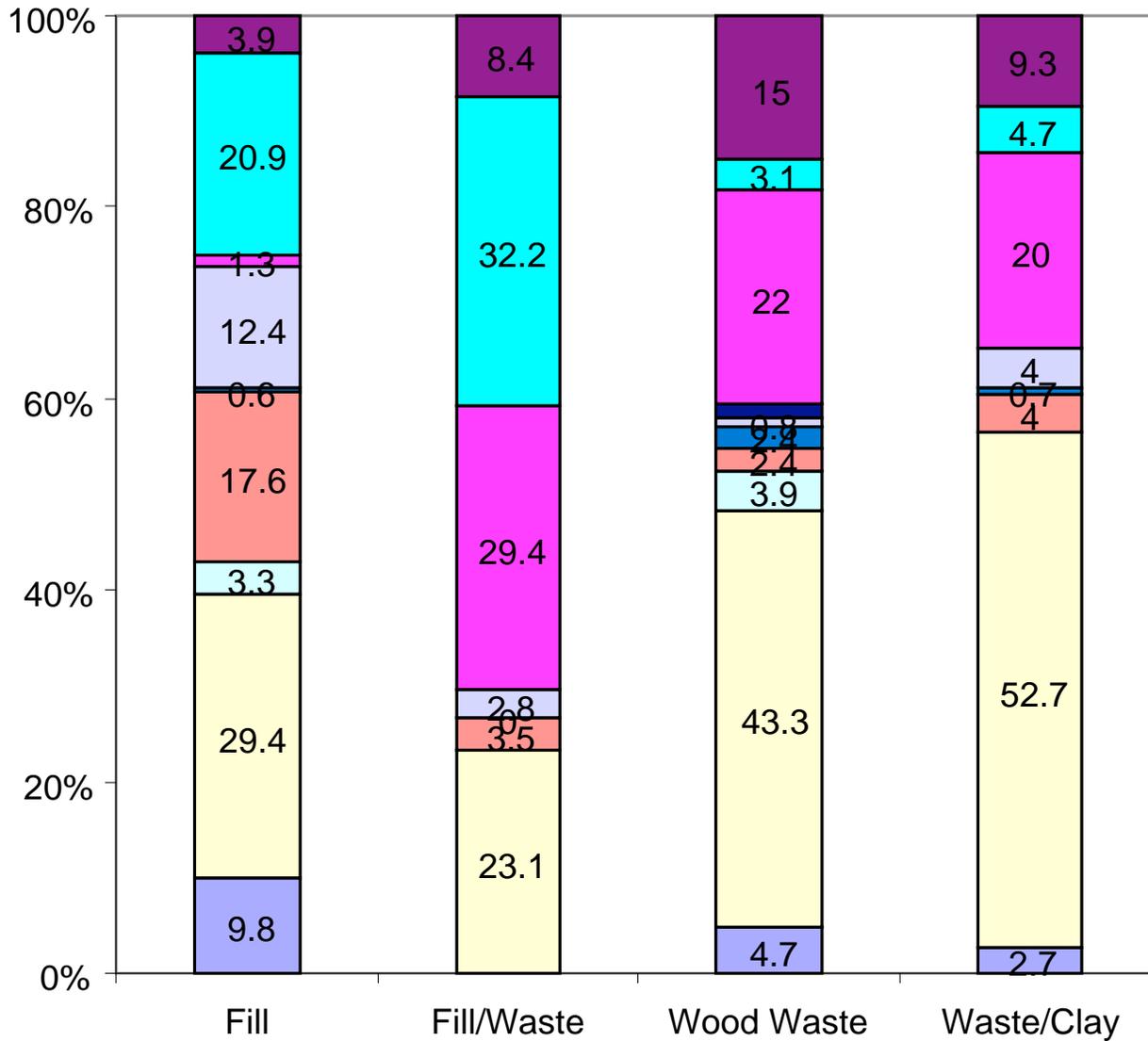
DOE Field Site Description



- INL Radioactive Waste Management Complex (RWMC) – Cold Test Pit South (CTPS)
- CTPS constructed in 1988, filled with simulated LLW waste that conforms to the historical disposal practices at the site – buried wood and cardboard.
- CTPS provides an environment to test innovative waste characterization and retrieval technology.

- DNA was extracted from each of these four layers for microbial community analysis.

Percentage Phyla in Each Soil Layer



- Acidobacteria
- Actinobacteria
- AD3
- Bacteroidetes
- Chlorobi
- Chloroflexis
- Firmicutes
- Gemmatimonadetes
- OP10
- Planctomycetes
- Proteobacteria
- Unclassified
- Verrucomicrobia



Microbial Community Analysis G2 Phylochip

Sent subsamples of each DNA extract (F, FW, WW, and WC) to Gary Anderson & Yvette Piceno (LBNL) for G2 Phylochip analysis (Brodie et al. 2006)



Comparison of Clone Library and Phylochip Diversity

Clone
Library

	# of Phyla	# of Classes	# of Orders	# of Families	OTUs
Fill	10(2)	18	29	45	151
Fill/Waste	7(0)	13	18	32	143
Wood/Waste	11(1)	19	36	48	127
Waste/Clay	11(1)	17	37	46	150

G2
Phylochip

	# of Phyla	# of Classes	# of Orders	# of Families	OTUs
Fill	30(7)	46	90	210	1630
Fill/Waste	33(9)	61	124	289	2056
Wood/Waste	30(8)	51	98	212	1984
Waste/Clay	28(7)	49	91	198	1925

() indicate number of candidate Phyla

	F	FW	WW	WC
Acidobacteria	62	65	24	21
Actinobacteria	157	218	219	175
Aquificae	1	2	2	1
Bacteroidetes	95	143	148	136
BRC1	0	3	0	0
Caldithrix	2	2	2	2
Chlamydiae	1	2	2	2
Chlorobi	13	11	11	11
Chloroflexi	35	35	38	31
Coprothermobacter	1	1	0	0
Cyanobacteria	7	38	49	49
Deferribacter	0	1	1	0
Deinococcus-Thermus	3	4	4	4
Dictyoglomi	1	1	1	1
Firmicutes	264	391	353	308
Gemmatimonadetes	9	13	13	12
Marine Group A	1	2	2	0
Natronoanaerobium	5	5	5	5
NC-10	4	4	4	4
Nitrospira	8	9	9	7
OP-10	7	8	7	15
OP3	3	3	0	0
OP8	2	2	0	0
OP9	0	3	0	0
Planctomycetes	18	23	23	23
Proteobacteria	805	969	970	934
Spirochaetes	34	35	37	36
Synergistes	9	3	9	6
TM-7	6	8	6	8
Thermodesulfobacteria	1	1	1	1
Thermotogae	0	1	1	1
Verrucomicrobia	20	25	28	27
WS3	3	3	3	0

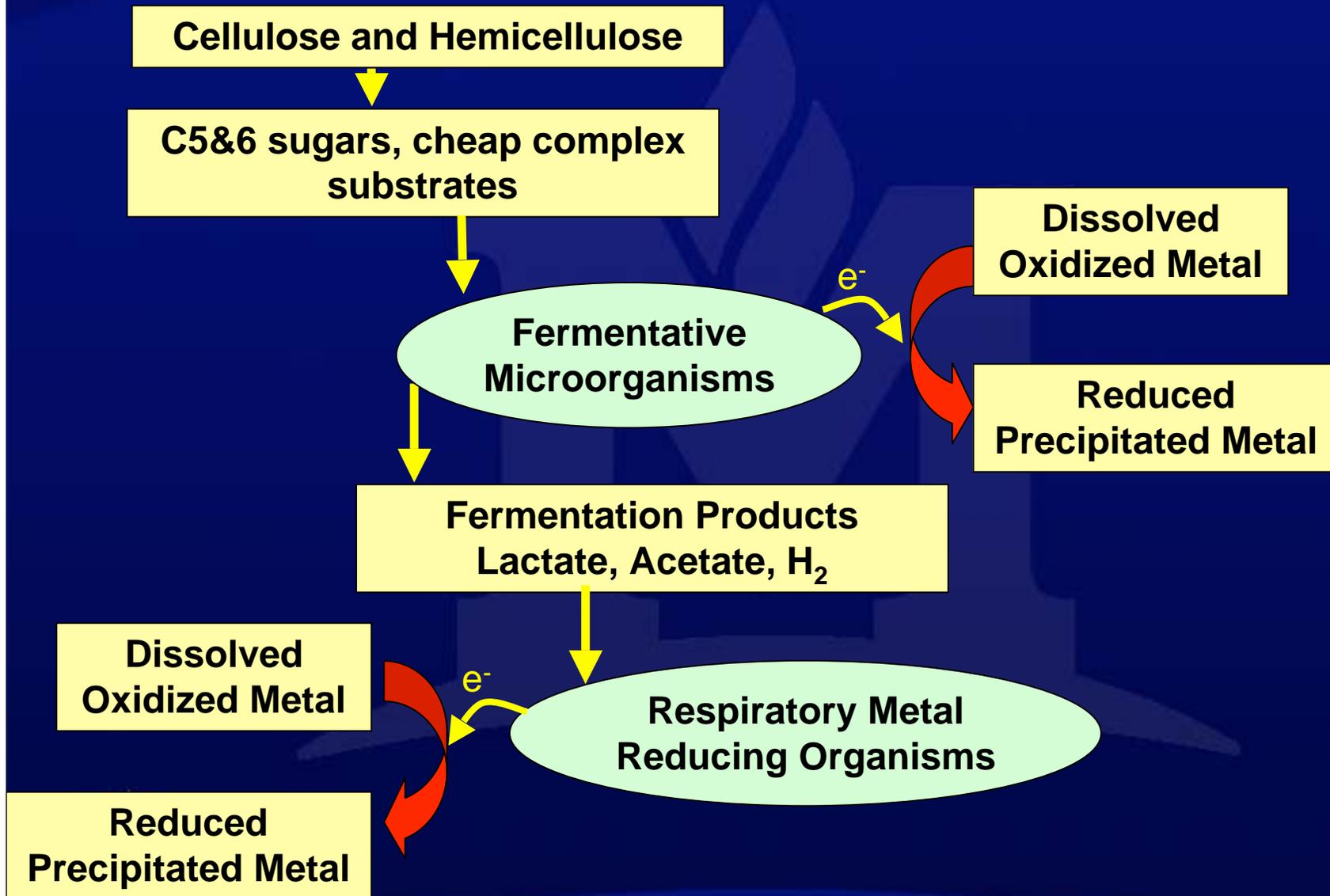
G2 Phylochip Results

- Rolled up to the Phylum level
- ~~Detailed physiology for each OTU?~~
- Translated into potential physiological capabilities, e.g., e- donor/acceptor combinations

CWTP Isolates

Isolate Designation	Genus of Isolate	Top BLAST Search Result	% Similarity to BLAST Result	O ₂ Requirements	Sources of Isolate
A	Pseudomonas	<i>Pseudomonas</i> sp. 4/11GC3#e	99	Aerobic	FW, WW, WC
B	Streptomyces	<i>Streptomyces</i> <i>atratus</i>	99	Aerobic	FW, WW, WC
C	Flavobacteria	<i>Flavobacterium</i> sp. WB 3.1 -83	98	Aerobic	FW, WW, WC
D	Pedobacter	<i>Pedobacter terrae</i>	99	Aerobic	WW
E	Serratia	<i>Serratia</i> <i>proteamaculans</i>	97	Facultative Anaerobe	FW
F	Cellulomonas	<i>Cellulomonas</i> <i>parahominis</i>	99	Facultative Anaerobe	FW, WW, WC
G	Paenibacillus	<i>Paenibacillus</i> sp. GP26-03	99	Facultative Anaerobe	WC

Fermentation - Metal Transformations



Summary

- Fermentative organisms have unique metal transformation capabilities and can play a significant role in subsurface Cr and U bio-immobilization.
- *Cellulomonas* sp. strain ES6 was shown to simultaneously immobilize U by reduction to U(IV) and by precipitation through release of PO_4^{3-} , with the ratio dependent on bicarbonate conc.
- ES6 reduced Cr(VI) for long periods of time with little substrate addition.
- Established fermenting communities are complex ... requiring modern tools to characterize – But we need to reduce the data to “functional physiologies” for modeling, and for field applications & monitoring.

Questions?

